

配列表

<110> SAITO, Koichi

<120> Estrogen receptor genes and uses thereof

<130> 561334

<150> JP 2002-004395

<151> 2002-01-11

<160> 48

<210> 1

<211> 506

<212> PRT

<213> Blue Gill

<400> 1

Met Ser Leu Lys Asp Trp Leu Leu Gly Lys Glu Arg Thr Val Val Thr

1 5 10 15

Met Glu Glu Leu Arg Ser Ser Val Pro Ser Ser Gln Gln Pro Val Pro

20 25 30

Arg Glu Asp Gln Cys Ala Thr Ser Asp Glu Ser Tyr Ser Val Gly Glu

| | | |
|---|-----|-----|
| 35 | 40 | 45 |
| Ser Gly Ala Gly Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg Phe | | |
| 50 | 55 | 60 |
| Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp | | |
| 65 | 70 | 75 |
| Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His | | |
| 85 | 90 | 95 |
| Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn | | |
| 100 | 105 | 110 |
| Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val | | |
| 115 | 120 | 125 |
| Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu Arg | | |
| 130 | 135 | 140 |
| Arg Asp Lys Arg Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser Lys | | |
| 145 | 150 | 155 |
| Asp Leu Glu Tyr Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His Ser | | |
| 165 | 170 | 175 |
| Ser Ser Ser Ser Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr Gly | | |
| 180 | 185 | 190 |
| Met Ser Pro Asp Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro Pro | | |
| 195 | 200 | 205 |
| Met Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr | | |
| 210 | 215 | 220 |
| Ile Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu Leu Val His Met | | |

| | | | |
|---|-----|-----|-----|
| 225 | 230 | 235 | 240 |
| Ile Thr Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His | | | |
| | 245 | 250 | 255 |
| Asp Gln Val Gln Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile | | | |
| | 260 | 265 | 270 |
| Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala | | | |
| | 275 | 280 | 285 |
| Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Phe | | | |
| | 290 | 295 | 300 |
| Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Met | | | |
| 305 | 310 | 315 | 320 |
| Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu | | | |
| | 325 | 330 | 335 |
| Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu | | | |
| | 340 | 345 | 350 |
| His Asn Ser Met Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp Ala | | | |
| | 355 | 360 | 365 |
| Leu Ile His His Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln Ser | | | |
| | 370 | 375 | 380 |
| Arg Arg Gln Ala Gln Leu Leu Leu Leu Leu Ser His Ile Arg His Met | | | |
| 385 | 390 | 395 | 400 |
| Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys | | | |
| | 405 | 410 | 415 |
| Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Ile | | | |

420 425 430
 His Arg Pro Asp Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly Glu
 435 440 445
 Pro Pro Phe Ile Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn Gly
 450 455 460
 Gly Val Ser Ser Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn His
 465 470 475 480
 Glu Ser Pro Ser Arg Gly Pro Thr Gly Pro Gly Val Leu Gln Tyr Gly
 485 490 495
 Gly Ser Arg Ser Asp Cys Thr His Ile Leu
 500 505

<210> 2

<211> 3499

<212> DNA

<213> Blue Gill

<220>

<221> CDS

<222> (424)... (1944)

<400> 2

caggcagagc ccagcgcaga gcagacagcc ttgtggaaca gtactcagac ccaggatcag 60
 ctcagccttc acagagctgg agaccctctc cccacaacgt ccctcgcctc cgctgcgtgc 120

| | |
|--|-----|
| ccctctcagt gacatgtacc ctgaagagag caggggggtcc ggaggggtag ccactgtgga | 180 |
| ctttctggaa gggacctacg attatgccgc cccaccct gccccgactc ctctttacag | 240 |
| ccagtctggc tactactctg tacctctgga cgcccaaggg ccaccctcag atggcagcct | 300 |
| tcagtccttg ggcagcgggc ctaccagtcc tcttgtgttt gtcccgcca gccccagact | 360 |
| cagccccctt atgcaccgc ccagccacca ctatctggaa accacctcaa caccgtcta | 420 |
| cag atg agt ctg aaa gac tgg tta tta gga aaa gaa agg acg gtg gtg | 468 |
| Met Ser Leu Lys Asp Trp Leu Leu Gly Lys Glu Arg Thr Val Val | |
| 1 5 10 15 | |
| acc atg gag gag ctg agg tct agt gtc cca tcc agc cag cag cca gtt | 516 |
| Thr Met Glu Glu Leu Arg Ser Ser Val Pro Ser Ser Gln Gln Pro Val | |
| 20 25 30 | |
| ccc aga gag gac cag tgt gcc acc agt gat gag tcc tat agt gtg ggg | 564 |
| Pro Arg Glu Asp Gln Cys Ala Thr Ser Asp Glu Ser Tyr Ser Val Gly | |
| 35 40 45 | |
| gag tca ggg gct gga gcc agg ggg ttt gag atg gcc aag gag atg cgt | 612 |
| Glu Ser Gly Ala Gly Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg | |
| 50 55 60 | |
| ttc tgt gct gtg tgc agt gac tat gcc tct ggg tac cac tac ggg gtg | 660 |
| Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val | |
| 65 70 75 | |
| tgg tcc tgt gaa ggc tgt aag gcc ttc ttt aag agg agc atc cag ggt | 708 |
| Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly | |
| 80 85 90 95 | |
| cac aat gac tat atg tgc cca gca acc aat cag tgt act att gac agg | 756 |

| | |
|---|------|
| His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg | |
| 100 105 110 | |
| aat cgg aga aag agc tgc cag gct tgc cgt ctt agg aag tgt tat gaa | 804 |
| Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu | |
| 115 120 125 | |
| gtg ggc atg atg aaa gga ggt gtt cgc aag gac cgt ggc cgt gtt ttg | 852 |
| Val Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu | |
| 130 135 140 | |
| cgc cgt gat aaa cga cgt gct gga acc aat gac cga gag aag gcc tct | 900 |
| Arg Arg Asp Lys Arg Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser | |
| 145 150 155 | |
| aag gac ctg gag tac aaa aca gtg ccc cct cag gac agg agg aaa cac | 948 |
| Lys Asp Leu Glu Tyr Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His | |
| 160 165 170 175 | |
| agc agc agc agc agt gcc ggt ggt gga gga gga aaa tca tca gtg acc | 996 |
| Ser Ser Ser Ser Ser Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr | |
| 180 185 190 | |
| ggg atg tct cct gac cag gtg ctc ctc ctg ctc cag ggt gcc gag ccc | 1044 |
| Gly Met Ser Pro Asp Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro | |
| 195 200 205 | |
| cca atg ctg tgc tcc cgt cag aag ctg agc cga ccg tac acc gag gtc | 1092 |
| Pro Met Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val | |
| 210 215 220 | |
| acc ata atg aca cta ctc acc agc atg gcc gat aag gag ctg gtc cac | 1140 |

| | |
|---|------|
| Thr Ile Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu Leu Val His | |
| 225 | 230 |
| atg atc acc tgg gcc aag aag ctt cca ggt ttc ctg cag ctg tct ctc | 1188 |
| Met Ile Thr Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu | |
| 240 | 245 |
| cat gac cag gtg cag ctg ctg gag agc tcg tgg ctg gag gtg ctg atg | 1236 |
| His Asp Gln Val Gln Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met | |
| 260 | 265 |
| att ggg ctc ata tgg agg tcc atc cac tgc ccc ggc aaa ctc atc ttc | 1284 |
| Ile Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe | |
| 275 | 280 |
| gca cag gac ctc ata ctg gac agg aat gaa ggt gac tgt gtg gaa ggc | 1332 |
| Ala Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly | |
| 290 | 295 |
| ttt gtt gag atc ttc gac atg ctg ctg gcc act gcc tcc cgc ttc cgc | 1380 |
| Phe Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg | |
| 305 | 310 |
| atg ctc aaa ctc aaa cct gag gag ttt gtc tgc ctc aaa gct atc atc | 1428 |
| Met Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile | |
| 320 | 325 |
| ctg ctc aac tct ggt gcc ttc tct ttc tgc acc ggc aca atg gag ccc | 1476 |
| Leu Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro | |
| 340 | 345 |
| ctc cac aac agc atg gca gtg cag aac atg ctg gac acc atc aca gac | 1524 |

Leu His Asn Ser Met Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp
 355 360 365
 gct ctc ata cat cat atc agc caa tca gga tgc tcg gct cag cag cag 1572
 Ala Leu Ile His His Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln
 370 375 380
 tcg agg cgg cag gcc cag ctg ctg ctc ctg ctc tcc cac atc agg cac 1620
 Ser Arg Arg Gln Ala Gln Leu Leu Leu Leu Leu Ser His Ile Arg His
 385 390 395
 atg agc aac aaa ggc atg gag cat ctc tac agc atg aag tgc aag aac 1668
 Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn
 400 405 410 415
 aaa gtg cct ctt tac gac ctt ctg ctg gag atg ttg gac gct cac cgt 1716
 Lys Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg
 420 425 430
 ata cac cgc cca gac aga cca gct cag ttc tgg tcc cag gct gac gga 1764
 Ile His Arg Pro Asp Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly
 435 440 445
 gag cct ccc ttc att aac aac aac aac agc agc aac agt ggc agc aat 1812
 Glu Pro Pro Phe Ile Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn
 450 455 460
 ggc ggc gtc tcc tct tca gtc ggt tcc agt tca gga ccc cga gtc aac 1860
 Gly Gly Val Ser Ser Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn
 465 470 475
 cac gag agc ccg agc aga gga ccc aca ggt cca gga gtc ctg cag tac 1908

His Glu Ser Pro Ser Arg Gly Pro Thr Gly Pro Gly Val Leu Gln Tyr
 480 485 490 495
 gga ggg tcc cgc tct gac tgc acc cac atc cta tga ggccgagcac aacaaa 1960
 Gly Gly Ser Arg Ser Asp Cys Thr His Ile Leu
 500 505
 catctgaagg tcaaaagtaa tttttacaga tgatgtgtgt tgtacagaat gaaagctaaa 2020
 gggtgtatgt taattaatgt catgagataa ttatttataa attaatgat tttatagttg 2080
 taactgtttt agggagtttt ttttcctttg cactaatcta gttcactaca acacgagctt 2140
 caatgcaggc aatctactat gctgcctttc ataatatctg tgattctgag tgagtacagc 2200
 ttaatttttc caggtgtag gtcattattgt ggcaactcagc tatggtgatt tgaaatgaca 2260
 agcagctaatt ttgcctttgt atttgcctca accaaagtgc acttcttctt gggtttattg 2320
 ggcatgtttt ttacttttac atattgggat taggatgatc agacactaaa ctatgataaa 2380
 aaacaggttc aaatgaatgt gtgatttatt ttgtgtttta attccaacat cattaaagag 2440
 cctgaacgtc aggtattgtg tcttaagcgt gcacgcaaac tttaaacttc tggaaaacaa 2500
 atatttctat gatgaaatta taaaattaac agtgattgag gatgtatgtt gaattcagag 2560
 tagatacaat ttgcacaatc aaatcctaga gcactgatca cattatgaaa gaagcaaagc 2620
 tttcacaact ttattgttgg gtaacttcac cacatccagc tttttgtgaa tggtaggttt 2680
 gttctgtagg cttacatgca caagagtttt ttttctgaat ttgagatatt ttatgtgtgt 2740
 ctgcaagaga aagactgaga aatctgagga aatttgctat aagtggcctt aagctttcta 2800
 tcttgatgca gttcagaatt tcaaaatgtt actattcatc cactaattca gtgattacat 2860
 gttgagtttg gcttgattta cacaactcca aaagcctagt taccattaaa tatgtgcata 2920
 tgcaattgtt tttattttgt ttaaattgaa caaatttaaat ctaaatctaa tatggacctg 2980
 accaggtgtt ttctttatta gctgctatac actgctaagc accattgtta atagtttgg 3040
 ttatatagct aaatagcttt ttccatgacc atcaaaggcc tccaaaagaa agctaattgt 3100

ctttcctaatt tctgtgataa acagactcca aaatcacact ggatgggtcac tgaacaagtc 3160
ctgcttcatg tttgtttaca tgtcaaccag caacgtcagc acacctgtgc tgttttgtat 3220
cctcccatga acagttgttc agtcacaggt ttgtcacaca ggtagaacia tctgttaata 3280
tactgaaaaa aaggccagag gttgacgtgt agagaatgtt gccagaatac aaatgataaa 3340
caaagatctg tgccacttaa acaagaatgg aaagcctcta tacagggtca ggaaactgga 3400
tttgacact tgaagtcaa gtcaaacctg acctgtcctc tgtttactgt gcataaaaaat 3460
aaaaacatta attgggaaaa aaaaaaaaaa aaaaaaaaaa 3499

<210> 3

<211> 996

<212> DNA

<213> Blue Gill

<400> 3

aggagcatcc aaggtcacaa tgactacatg tgcccagcaa ccaatcagtg tactattgac 60
aggaatcgga gaaagagctg ccaggcttgc cgtcttagga agtggtatga agtgggcatg 120
atgaaaggag gtgttcgcaa ggaccgtggc cgtgttttgc gccgtgataa acgacgtgct 180
ggaaccaatg accgagagaa ggcttctaag gacctggagt aaaaaacagt gccccctcag 240
gacaggagga aacacagcag cagcagcagt gccggtgggtg gaggaggaaa atcatcagtg 300
accgggatgt ctcctgacca ggtgctcttc ctgctccagg gtgccgagcc ccaatgctg 360
tgctcccgtc agaagctgag ccgaccgtac accgaggtca ccataatgac actactcacc 420
agcatggccg ataaggagct ggtccacatg atcacctggg ccaagaagct tccaggtttc 480
ctgcagctgt ctctccatga ccaggtgcag ctgctggaga gctcgtggct ggaggtgctg 540
atgattgggc tcatatggag gtccatccac tgccccggca aactcatctt cgcacaggac 600

His Pro Pro Ser His His Tyr Leu Glu Thr Thr Ser Thr Pro Val Tyr
85 90 95

Arg Ser Ser Val Pro Ser Ser Gln Gln Pro Val Pro Arg Glu Asp Gln
100 105 110

Cys Ala Thr Ser Asp Glu Ser Tyr Ser Val Gly Glu Ser Gly Ala Gly
115 120 125

Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg Phe Cys Ala Val Cys
130 135 140

Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly
145 150 155 160

Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met
165 170 175

Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn Arg Arg Lys Ser
180 185 190

Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys
195 200 205

Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu Arg Arg Asp Lys Arg
210 215 220

Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser Lys Asp Leu Glu Tyr
225 230 235 240

Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His Ser Ser Ser Ser Ser
245 250 255

Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr Gly Met Ser Pro Asp
260 265 270

Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro Pro Met Leu Cys Ser
275 280 285

Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr Ile Met Thr Leu
290 295 300

Leu Thr Ser Met Ala Asp Lys Glu Leu Val His Met Ile Thr Trp Ala
305 310 315 320

Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His Asp Gln Val Gln
325 330 335

Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile Gly Leu Ile Trp
340 345 350

Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala Gln Asp Leu Ile
355 360 365

Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Phe Val Glu Ile Phe
370 375 380

Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Met Leu Lys Leu Lys
385 390 395 400

Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu Leu Asn Ser Gly
405 410 415

Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu His Asn Ser Met
420 425 430

Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp Ala Leu Ile His His
435 440 445

Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln Ser Arg Arg Gln Ala
450 455 460

Gln Leu Leu Leu Leu Leu Ser His Ile Arg His Met Ser Asn Lys Gly
 465 470 475 480
 Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys Val Pro Leu Tyr
 485 490 495
 Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Ile His Arg Pro Asp
 500 505 510
 Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly Glu Pro Pro Phe Ile
 515 520 525
 Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn Gly Gly Val Ser Ser
 530 535 540
 Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn His Glu Ser Pro Ser
 545 550 555 560
 Arg Gly Pro Thr Gly Pro Gly Val Leu Gln Tyr Gly Gly Ser Arg Ser
 565 570 575
 Asp Cys Thr His Ile Leu
 580

<210> 5

<211> 1824

<212> DNA

<213> Blue Gill

<220>

<221> CDS

<222> (74)... (1822)

<400> 5

| | |
|--|-----|
| ctcagccttc acagagctgg agaccctctc cccacaacgt ccctcgccctc cgctgcgtgc | 60 |
| ccctctcagt gac atg tac cct gaa gag agc agg ggg tcc gga ggg gta | 109 |
| Met Tyr Pro Glu Glu Ser Arg Gly Ser Gly Gly Val | |
| 1 5 10 | |
| gcc act gtg gac ttt ctg gaa ggg acc tac gat tat gcc gcc ccc acc | 157 |
| Ala Thr Val Asp Phe Leu Glu Gly Thr Tyr Asp Tyr Ala Ala Pro Thr | |
| 15 20 25 | |
| cct gcc ccg act cct ctt tac agc cag tct ggc tac tac tct gta cct | 205 |
| Pro Ala Pro Thr Pro Leu Tyr Ser Gln Ser Gly Tyr Tyr Ser Val Pro | |
| 30 35 40 | |
| ctg gac gcc caa ggg cca ccc tca gat ggc agc ctt cag tcc ctg ggc | 253 |
| Leu Asp Ala Gln Gly Pro Pro Ser Asp Gly Ser Leu Gln Ser Leu Gly | |
| 45 50 55 60 | |
| agc ggg cct acc agt cct ctt gtg ttt gtg ccg tcc agc ccc aga ctc | 301 |
| Ser Gly Pro Thr Ser Pro Leu Val Phe Val Pro Ser Ser Pro Arg Leu | |
| 65 70 75 | |
| agc ccc ttt atg cac ccg ccc agc cac cac tat ctg gaa acc acc tca | 349 |
| Ser Pro Phe Met His Pro Pro Ser His His Tyr Leu Glu Thr Thr Ser | |
| 80 85 90 | |
| aca ccc gtc tac agg tct agt gtc cca tcc agc cag cag cca gtt ccc | 397 |
| Thr Pro Val Tyr Arg Ser Ser Val Pro Ser Ser Gln Gln Pro Val Pro | |

| | | | |
|---|-----|-----|-----|
| 95 | 100 | 105 | |
| aga gag gac cag tgt gcc acc agt gat gag tcc tat agt gtg ggg gag | | | 445 |
| Arg Glu Asp Gln Cys Ala Thr Ser Asp Glu Ser Tyr Ser Val Gly Glu | | | |
| 110 | 115 | 120 | |
| tca ggg gct gga gcc agg ggg ttt gag atg gcc aag gag atg cgt ttc | | | 493 |
| Ser Gly Ala Gly Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg Phe | | | |
| 125 | 130 | 135 | 140 |
| tgt gct gtg tgc agt gac tat gcc tct ggg tac cac tac ggg gtg tgg | | | 541 |
| Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp | | | |
| 145 | 150 | 155 | |
| tcc tgt gaa ggc tgt aag gcc ttc ttt aag agg agc atc cag ggt cac | | | 589 |
| Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His | | | |
| 160 | 165 | 170 | |
| aat gac tat atg tgc cca gca acc aat cag tgt act att gac agg aat | | | 637 |
| Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn | | | |
| 175 | 180 | 185 | |
| cgg aga aag agc tgc cag gct tgc cgt ctt agg aag tgt tat gaa gtg | | | 685 |
| Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val | | | |
| 190 | 195 | 200 | |
| ggc atg atg aaa gga ggt gtt cgc aag gac cgt ggc cgt gtt ttg cgc | | | 733 |
| Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu Arg | | | |
| 205 | 210 | 215 | 220 |
| cgt gat aaa cga cgt gct gga acc aat gac cga gag aag gcc tct aag | | | 781 |
| Arg Asp Lys Arg Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser Lys | | | |

| | | | |
|---|-----|-----|------|
| 225 | 230 | 235 | |
| gac ctg gag tac aaa aca gtg ccc cct cag gac agg agg aaa cac agc | | | 829 |
| Asp Leu Glu Tyr Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His Ser | | | |
| 240 | 245 | 250 | |
| agc agc agc agt gcc ggt ggt gga gga gga aaa tca tca gtg acc ggg | | | 877 |
| Ser Ser Ser Ser Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr Gly | | | |
| 255 | 260 | 265 | |
| atg tct cct gac cag gtg ctc ctc ctg ctc cag ggt gcc gag ccc cca | | | 925 |
| Met Ser Pro Asp Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro Pro | | | |
| 270 | 275 | 280 | |
| atg ctg tgc tcc cgt cag aag ctg agc cga ccg tac acc gag gtc acc | | | 973 |
| Met Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr | | | |
| 285 | 290 | 295 | 300 |
| ata atg aca cta ctc acc agc atg gcc gat aag gag ctg gtc cac atg | | | 1021 |
| Ile Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu Leu Val His Met | | | |
| 305 | 310 | 315 | |
| atc acc tgg gcc aag aag ctt cca ggt ttc ctg cag ctg tct ctc cat | | | 1069 |
| Ile Thr Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His | | | |
| 320 | 325 | 330 | |
| gac cag gtg cag ctg ctg gag agc tcg tgg ctg gag gtg ctg atg att | | | 1117 |
| Asp Gln Val Gln Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile | | | |
| 335 | 340 | 345 | |
| ggg ctc ata tgg agg tcc atc cac tgc ccc ggc aaa ctc atc ttc gca | | | 1165 |
| Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala | | | |

| | | | |
|---|-----|-----|------|
| 350 | 355 | 360 | |
| cag gac ctc ata ctg gac agg aat gaa ggt gac tgt gtg gaa ggc ttt | | | 1213 |
| Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Phe | | | |
| 365 | 370 | 375 | 380 |
| gtt gag atc ttc gac atg ctg ctg gcc act gcc tcc cgc ttc cgc atg | | | 1261 |
| Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Met | | | |
| 385 | 390 | 395 | |
| ctc aaa ctc aaa cct gag gag ttt gtc tgc ctc aaa gct atc atc ctg | | | 1309 |
| Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu | | | |
| 400 | 405 | 410 | |
| ctc aac tct ggt gcc ttc tct ttc tgc acc ggc aca atg gag ccc ctc | | | 1357 |
| Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu | | | |
| 415 | 420 | 425 | |
| cac aac agc atg gca gtg cag aac atg ctg gac acc atc aca gac gct | | | 1405 |
| His Asn Ser Met Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp Ala | | | |
| 430 | 435 | 440 | |
| ctc ata cat cat atc agc caa tca gga tgc tcg gct cag cag cag tcg | | | 1453 |
| Leu Ile His His Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln Ser | | | |
| 445 | 450 | 455 | 460 |
| agg cgg cag gcc cag ctg ctg ctc ctg ctc tcc cac atc agg cac atg | | | 1501 |
| Arg Arg Gln Ala Gln Leu Leu Leu Leu Leu Ser His Ile Arg His Met | | | |
| 465 | 470 | 475 | |
| agc aac aaa ggc atg gag cat ctc tac agc atg aag tgc aag aac aaa | | | 1549 |
| Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys | | | |

| | | | |
|---|-----|-----|------|
| 480 | 485 | 490 | |
| gtg cct ctt tac gac ctt ctg ctg gag atg ttg gac gct cac cgt ata | | | 1597 |
| Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Ile | | | |
| 495 | 500 | 505 | |
| cac cgc cca gac aga cca gct cag ttc tgg tcc cag gct gac gga gag | | | 1645 |
| His Arg Pro Asp Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly Glu | | | |
| 510 | 515 | 520 | |
| cct ccc ttc att aac aac aac aac agc agc aac agt ggc agc aat ggc | | | 1693 |
| Pro Pro Phe Ile Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn Gly | | | |
| 525 | 530 | 535 | 540 |
| ggc gtc tcc tct tca gtc ggt tcc agt tca gga ccc cga gtc aac cac | | | 1741 |
| Gly Val Ser Ser Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn His | | | |
| 545 | 550 | 555 | |
| gag agc ccg agc aga gga ccc aca ggt cca gga gtc ctg cag tac gga | | | 1789 |
| Glu Ser Pro Ser Arg Gly Pro Thr Gly Pro Gly Val Leu Gln Tyr Gly | | | |
| 560 | 565 | 570 | |
| ggg tcc cgc tct gac tgc acc cac atc cta tga gg | | | 1824 |
| Gly Ser Arg Ser Asp Cys Thr His Ile Leu | | | |
| 575 | 580 | | |

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 6

cccagcgcag agcagacagc cttgtggaac 30

<210> 7

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 7

cttttgacct tcagatgttt gttgtgctcg 31

<210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 8

aggagcatcc aaggtcaca tgactac 27

<210> 9

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 9

caggtcgtac agaggcactt tggtcttg 28

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 10

tctggctact actctgtacc tctg 24

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 11

ccccacacta taggactcat catc 24

<210> 12

<211> 62

<212> DNA

<213> Blue Gill

<400> 12

atgagtctga aagactgggtt attaggaaaa gaaaggacgg tggtagcat ggaggagctg 60

ag

62

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 13

gagcagacag ccttgtggaa cagt 24

<210> 14

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 14

gcctctagac caccatgagt ctgaaagact ggttattag 39

<210> 15

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 15

gcctctagag ttgtgctcgg cctcatagga tgtgggtgc 39

<210> 16

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 16

ggcaagcttc caccatgtac cctgaagaga gcaggggg 38

<210> 17

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for synthesis of promoter DNA

<400> 17

gatctcgact ataaagaggg caggctgtcc tctaagcgtc accacgactt ca 52

<210> 18

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for synthesis of promoter DNA

<400> 18

agcttgaagt cgtggtgacg cttagaggac agcctgccct ctttatagtc ga 52

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 19

ggccgaattc ggcatgatga aaggaggtgt tcgc 34

<210> 20

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 20

ggccgtcgac gtgctcggcc tcataggatgt ggg 33

<210> 21

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 21

gccgaattcg agagagctga cgggcagagc aga 33

<210> 22

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 22

gccagatctg ctcatagttg ctggcatacc act 33

<210> 23

<211> 554

<212> PRT

<213> Blue gill

<400> 23

Met Ala Cys Ser Pro Glu Lys Asp Gln Pro Leu Leu Gln Leu Gln Lys

1

5

10

15

Val Asp Ser Ser Arg Val Gly Ser Arg Val Val Ser Pro Ile Leu Asn

20

25

30

Ser Pro Leu Glu Arg Ser Gln Pro Ile Cys Ile Pro Ser Pro Tyr Thr
35 40 45

Asp Leu Ser His Asp Phe Thr Thr Ile Pro Phe Tyr Ser Pro Thr Phe
50 55 60

Phe Ser Tyr Ala Ser Pro Gly Ile Ser Asp Cys Pro Ser Val His Gln
65 70 75 80

Ser Leu Ser Pro Ser Leu Phe Trp Pro Ser His Gly His Val Gly Ser
85 90 95

Pro Ile Pro Leu His His Ser Gln Pro Arg Pro Gln His Arg Gln Pro
100 105 110

Ile Gln Ser Pro Trp Val Glu Leu Ser Pro Leu Glu Ser Thr Leu Thr
115 120 125

Thr Ser Lys Ser Val Arg Arg Arg Ser Gln Glu Ser Glu Asp Gly Val
130 135 140

Val Ser Ser Gly Gly Lys Ala Asp Ile His Tyr Cys Ala Val Cys His
145 150 155 160

Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys
165 170 175

Lys Ala Phe Phe Lys Arg Ser Ile Gln Arg His Asn Asp Tyr Ile Cys
180 185 190

Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys
195 200 205

Gln Ala Cys Arg Leu Arg Lys Cys Asn Glu Val Gly Met Thr Lys Cys
210 215 220

Gly Val Arg Lys Glu Arg Gly Asn Cys Arg Asn Pro Gln Met Arg Arg
225 230 235 240
Val Thr Arg Leu Ser Thr Gln Gly Arg Thr Asn Arg Thr Ala Val Leu
245 250 255
Thr Gly Pro Ala Val Gly Ser Leu Ile Ser Leu Asn Ser Pro Ala Leu
260 265 270
Thr Pro Glu Gln Leu Ile Glu Arg Ile Ile Asp Ala Glu Pro Pro Glu
275 280 285
Ile Tyr Leu Met Lys Asp Met Arg Arg Pro Leu Thr Glu Ala Asn Val
290 295 300
Met Met Ser Leu Thr Asn Leu Ala Asp Lys Glu Leu Val His Met Ile
305 310 315 320
Ser Trp Ala Lys Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Leu Asp
325 330 335
Gln Val His Leu Leu Glu Cys Cys Trp Leu Glu Val Leu Met Val Gly
340 345 350
Leu Met Trp Arg Ser Val Asp His Pro Gly Lys Leu Ile Phe Ser Arg
355 360 365
Asp Leu Ser Leu Ser Arg Glu Glu Gly Ser Cys Val Gln Gly Phe Ala
370 375 380
Glu Ile Phe Asp Met Leu Ile Ala Ala Thr Ser Arg Val Arg Glu Leu
385 390 395 400
Lys Leu Gln Arg Glu Glu Tyr Val Cys Leu Lys Ala Met Ile Leu Leu
405 410 415

Asn Ser Asn Met Cys Leu Gly Ser Ser Glu Gly Ser Glu Glu Leu Gln
420 425 430
Ser Arg Ser Lys Leu Leu Cys Leu Leu Asp Ala Val Thr Asp Ala Leu
435 440 445
Val Trp Ala Ile Ala Lys Thr Gly Leu Thr Phe Arg Gln Gln Tyr Thr
450 455 460
Arg Leu Ala His Leu Leu Met Leu Leu Ser His Ile Arg His Val Ser
465 470 475 480
Asn Lys Gly Met Asp His Leu His Cys Met Lys Met Lys Asn Met Val
485 490 495
Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Ile Met His
500 505 510
Ser Ser Arg Leu Ser His Gln Pro Ile Gln Gln Asp Ala Gln Asp Gln
515 520 525
Arg Glu Ala Pro Ala Arg Pro His Ser Cys Gly Ser Gly Pro Leu Asn
530 535 540
Thr Trp Thr Pro Gly Gly Gly Glu Arg Gln
545 550

<210> 24

<211> 2186

<212> DNA

<213> Blue gill

<220>

<221> CDS

<222> (106)...(1770)

<400> 24

cttacactga cactcggaga aaaagatgac taatgacatc ctaggcccat attctttgtc 60
gacgatgtgg tagatctagt gatactgaga cagtcagtag ttgca atg gcc tgc tct 117

Met Ala Cys Ser

1

cca gag aag gat cag ccc ctc ctc cag ctc cag aag gtg gac tcc agt 165
Pro Glu Lys Asp Gln Pro Leu Leu Gln Leu Gln Lys Val Asp Ser Ser

5 10 15 20

cga gtt ggc agt cgt gtc gtc tcc ccg atc ctc aac tcc ccg ttg gaa 213
Arg Val Gly Ser Arg Val Val Ser Pro Ile Leu Asn Ser Pro Leu Glu

25 30 35

aga agc cag ccc atc tgc atc ccc tcc cct tac acc gac ctc agc cac 261
Arg Ser Gln Pro Ile Cys Ile Pro Ser Pro Tyr Thr Asp Leu Ser His

40 45 50

gac ttc acc acc ata cct ttc tac agt cca act ttc ttt agt tat gcc 309
Asp Phe Thr Thr Ile Pro Phe Tyr Ser Pro Thr Phe Phe Ser Tyr Ala

55 60 65

agt cca ggc att tca gac tgc ccc tcc gtc cat cag tca cta agc ccc 357
Ser Pro Gly Ile Ser Asp Cys Pro Ser Val His Gln Ser Leu Ser Pro

70 75 80

tcc tta ttc tgg ccc agc cat ggc cat gtt ggg tcc ccc ata ccc ctg 405

Ser Leu Phe Trp Pro Ser His Gly His Val Gly Ser Pro Ile Pro Leu

85 90 95 100

cac cac tcc cag cct cga cct cag cac aga cag cca atc cag agt cca 453

His His Ser Gln Pro Arg Pro Gln His Arg Gln Pro Ile Gln Ser Pro

105 110 115

tgg gtg gag ttg tca cca ctg gag agc acc tta aca acc agt aag agt 501

Trp Val Glu Leu Ser Pro Leu Glu Ser Thr Leu Thr Thr Ser Lys Ser

120 125 130

gta agg agg cgt tct cag gag agc gag gat ggc gtg gtg tcg tcc ggc 549

Val Arg Arg Arg Ser Gln Glu Ser Glu Asp Gly Val Val Ser Ser Gly

135 140 145

ggg aag gcg gac atc cac tac tgc gct gtg tgt cac gac tac gcc tca 597

Gly Lys Ala Asp Ile His Tyr Cys Ala Val Cys His Asp Tyr Ala Ser

150 155 160

gga tac cac tac ggc gtc tgg tca tgt gag ggg tgt aag gcc ttc ttc 645

Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe

165 170 175 180

aag agg agc atc caa aga cac aat gac tac atc tgc cca gca acc aat 693

Lys Arg Ser Ile Gln Arg His Asn Asp Tyr Ile Cys Pro Ala Thr Asn

185 190 195

caa tgc act ata gac aag aac cgc cgt aag agc tgc cag gcg tgc cgc 741

Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg

| | | | |
|---|-----|-----|------|
| 200 | 205 | 210 | |
| ctt cgc aaa tgc aat gaa gtt ggc atg acc aag tgt ggt gtg aga aag | | | 789 |
| Leu Arg Lys Cys Asn Glu Val Gly Met Thr Lys Cys Gly Val Arg Lys | | | |
| 215 | 220 | 225 | |
| gag cgt ggg aac tgc aga aac ccc cag atg agg cga gtg acc cga ctc | | | 837 |
| Glu Arg Gly Asn Cys Arg Asn Pro Gln Met Arg Arg Val Thr Arg Leu | | | |
| 230 | 235 | 240 | |
| tcc aca cag ggc aga act aac aga aca gct gtg tta act gga cca gcc | | | 885 |
| Ser Thr Gln Gly Arg Thr Asn Arg Thr Ala Val Leu Thr Gly Pro Ala | | | |
| 245 | 250 | 255 | 260 |
| gtg ggt tca cta atc tcg ctc aac tct cct gca ctg acc cca gag cag | | | 933 |
| Val Gly Ser Leu Ile Ser Leu Asn Ser Pro Ala Leu Thr Pro Glu Gln | | | |
| 265 | 270 | 275 | |
| ctg att gaa cga ata att gat gct gag cca cca gag atc tac ctc atg | | | 981 |
| Leu Ile Glu Arg Ile Ile Asp Ala Glu Pro Pro Glu Ile Tyr Leu Met | | | |
| 280 | 285 | 290 | |
| aaa gac atg agg agg cct ctg act gaa gca aac gtc atg atg tcg ctc | | | 1029 |
| Lys Asp Met Arg Arg Pro Leu Thr Glu Ala Asn Val Met Met Ser Leu | | | |
| 295 | 300 | 305 | |
| aca aac ctt gct gat aag gag ctg gtt cac atg atc agc tgg gcc aag | | | 1077 |
| Thr Asn Leu Ala Asp Lys Glu Leu Val His Met Ile Ser Trp Ala Lys | | | |
| 310 | 315 | 320 | |
| aag att cca ggg ttt gta gag ctc agt ctc ttg gac cag gtg cac ctg | | | 1125 |
| Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Leu Asp Gln Val His Leu | | | |

| | | | | |
|---|-----|-----|-----|------|
| 325 | 330 | 335 | 340 | |
| ttg gag tgc tgc tgg ctg gag gtg ctg atg gtt gga ctg atg tgg agg | | | | 1173 |
| Leu Glu Cys Cys Trp Leu Glu Val Leu Met Val Gly Leu Met Trp Arg | | | | |
| | 345 | 350 | 355 | |
| tca gtg gac cat cct ggg aaa ctt atc ttc tcc cgg gac ctc agc ctg | | | | 1221 |
| Ser Val Asp His Pro Gly Lys Leu Ile Phe Ser Arg Asp Leu Ser Leu | | | | |
| | 360 | 365 | 370 | |
| agc aga gaa gag ggg agc tgt gtc cag ggc ttc gca gag atc ttt gat | | | | 1269 |
| Ser Arg Glu Glu Gly Ser Cys Val Gln Gly Phe Ala Glu Ile Phe Asp | | | | |
| | 375 | 380 | 385 | |
| atg ctg ata gct gcc acg tcc agg gtg aga gag ctc aag ctc cag agg | | | | 1317 |
| Met Leu Ile Ala Ala Thr Ser Arg Val Arg Glu Leu Lys Leu Gln Arg | | | | |
| | 390 | 395 | 400 | |
| gag gag tac gtc tgc ctc aag gcc atg atc ctc ctt aac tcc aac atg | | | | 1365 |
| Glu Glu Tyr Val Cys Leu Lys Ala Met Ile Leu Leu Asn Ser Asn Met | | | | |
| | 405 | 410 | 415 | 420 |
| tgc ctc ggc tcc tca gag ggc agc gag gag ctg cag agt cgc tcc aag | | | | 1413 |
| Cys Leu Gly Ser Ser Glu Gly Ser Glu Glu Leu Gln Ser Arg Ser Lys | | | | |
| | 425 | 430 | 435 | |
| ctg ctg tgt ctt ctg gac gct gta acg gac gct ctg gtg tgg gcc atc | | | | 1461 |
| Leu Leu Cys Leu Leu Asp Ala Val Thr Asp Ala Leu Val Trp Ala Ile | | | | |
| | 440 | 445 | 450 | |
| gcc aaa act ggc ctc act ttc cgc caa cag tac acc cgc ctc gcc cac | | | | 1509 |
| Ala Lys Thr Gly Leu Thr Phe Arg Gln Gln Tyr Thr Arg Leu Ala His | | | | |

| | | | |
|--|-----|-----|------|
| 455 | 460 | 465 | |
| ctg ctt atg ctg ctc tca cac atc cgc cat gtc agt aac aaa ggc atg | | | 1557 |
| Leu Leu Met Leu Leu Ser His Ile Arg His Val Ser Asn Lys Gly Met | | | |
| 470 | 475 | 480 | |
| gac cac ctc cac tgc atg aaa atg aag aac atg gtg cct ttg tat gac | | | 1605 |
| Asp His Leu His Cys Met Lys Met Lys Asn Met Val Pro Leu Tyr Asp | | | |
| 485 | 490 | 495 | 500 |
| ctg ctg ctg gag atg ttg gat gcc cac atc atg cac agc tcc cgt ctg | | | 1653 |
| Leu Leu Leu Glu Met Leu Asp Ala His Ile MET His Ser Ser Arg Leu | | | |
| 505 | 510 | 515 | |
| tct cac cag ccc ata cag caa gac gca cag gac cag agg gag gct cct | | | 1701 |
| Ser His Gln Pro Ile Gln Gln Asp Ala Gln Asp Gln Arg Glu Ala Pro | | | |
| 520 | 525 | 530 | |
| gct cgg cca cac agc tgt gga agc ggc cct tta aac acc tgg aca cca | | | 1749 |
| Ala Arg Pro His Ser Cys Gly Ser Gly Pro Leu Asn Thr Trp Thr Pro | | | |
| 535 | 540 | 545 | |
| ggt gga ggt gaa cgg cag tag tctgatggaa tgaattttca ccgctttgca caaa | | | 1804 |
| Gly Gly Gly Glu Arg Gln | | | |
| 550 | | | |
| actacttcac aaaactgatg agatgtttca cttgaacatt cttcagcacg cttaaattctg | | | 1864 |
| tgaaactcga gctttgacac actgtgcact acttatattg aacttttttg aatatctaaa | | | 1924 |
| gtttttcatt tgttattcat tgccttacca ccacatattg aaaagccagc aaacagatta | | | 1984 |
| agcagttgct gttataattg ggccagtagc acaattagtt gctcatatgt tcaggtaata | | | 2044 |
| tgttactgcc gtgaatctcc tgggtcgagc agctaatttc ctatcaaata acattgataa | | | 2104 |

ataacattgt gtggaagga gagacagtat ggtttcacct gtcacagtaa cacctgaggc 2164
agatcctgag atggtgttac ct 2186

<210> 25

<211> 963

<212> DNA

<213> Blue gill

<400> 25

aggagcatcc aaggtcacaa tgactacatc tgcccagcaa ccaatcaatg cactatagac 60
aagaaccgcc gtaagagctg ccaggcgtgc cgccttcgca aatgcaatga agttggcatg 120
accaagtgtg gtgtgagaaa ggagcgtggg aactgcagaa acccccagat gaggcgagtg 180
acccgactct ccacacaggg cagaactaac agaacagctg tgtaactgg accagccgtg 240
ggttcactaa tctcgtcaa ctctcctgca ctgaccccag agcagctgat tgaacgaata 300
attgatgctg agccaccaga gatctacctc atgaaagaca tgaggaggcc tctgactgaa 360
gcaaacgtca tgatgtcgt cacaacctt gctgataagg agctgggtca catgatcagc 420
tgggccaaga agattccagg gttttagag ctgagctctt tggaccaggt gcacctgttg 480
gagtgtgct ggctggaggt gctgatggtt ggactgatgt ggaggtcagt ggaccatcct 540
gggaaactta tcttctcccg ggacctcagc ctgagcagag aagaggggag ctgtgtccag 600
ggcttcgcag agatctttga tatgctgata gctgccacgt ccagggtgag agagctcaag 660
ctccagaggg aggagtacgt ctgcctcaag gccatgatcc tccttaactc caacatgtgc 720
ctcggctcct cagagggcag cgaggagctg cagagtcgt ccaagctgct gtgtcttctg 780
gacgctgtaa cggacgctct ggtgtgggcc atcgccaaaa ctggcctcac tttccgcca 840
cagtacaccc gcctcgccca cctgcttatg ctgctctcac acatccgcca tgtcagtaac 900

aaaggcatgg accacctcca ctgcatgaaa atgaacaaga acaaagtgcc tctgtacgac 960

ctg

963

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 26

gatactgaga cagtcagtag ttgca 25

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 27

tgcaaagcgg tgaaaattca ttccat 26

<210> 28

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 28

aggagcatcc aaggtcacia tgactac 27

<210> 29

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 29

caggtcgtac agaggcactt tgttcttg 28

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 30

ctaggcccat attctttgtc gacgatgt 28

<210> 31

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 31

ataagtagtg cacagtgtgt caaagct 27

<210> 32

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to synthesize promoter DNA

<400> 32

gatctcgact ataaagaggg caggctgtcc tctaagcgtc accacgactt ca 52

<210> 33

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to synthesize promoter DNA

<400> 33

agcttgaagt cgtggtgacg cttagaggac agcctgccct ctttatagtc ga 52

<210> 34

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 34

gccgaattcg gcatgaccaa gtgtggt 27

<210> 35

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 35

ccggtcgacc tactgccgtt cacctccacc 30

<210> 36

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 36

gccgaattcg agagagctga cgggcagagc aga 33

<210> 37

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 37

gccagatctg ctcatagttg ctggcatacc act 33

<210> 38

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 38

agagtcgggt cactcgcctc atctg 25

<210> 39

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 39

gtctatagtg cattgattgg ttgct 25

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 40

tgacacacag cgcagtagtg 20

<210> 41

<211> 494

<212> DNA

<213> Blue gill

<400> 41

```

gtcgacgatg tggtagatct agtgatactg agacagtcag tagttgcaat ggcctgctct      60
ccagagaagg atcagcccct cctccagctc cagaagggtg actccagtcg agttggcagt      120
cgtgtcgtct ccccgatcct caactccccg ttggaagaag ccagcccata tgcataccct      180
ccccttacac cgacctcagc cagcacttca ccaccatacc tttctacagt ccaactttct      240
ttagttatgc cagtcaggc atttcagact gccctccgt ccatcagtc ctaagcccct      300
ccttattctg gccagccat ggccatgttg ggtcccccat acccctgcac cactcccagc      360
ctcgacctca gcacagacag ccaatccaga gtccatgggt ggagttgtca cactggaga      420
gcaccttaac aaccagtaag agtgtaagga ggcgttctca ggagagcgag gatggcgttg      480
tgctgtccgg cggg

```

494

<210> 42

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 42

gtctgaaatg cctggactgg ca 22

<210> 43

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 43

actggagtcc accttctgga g 21

<210> 44

<211> 139

<212> DNA

Blue gill

<400> 44

cttacactga cactcggaga aaaagatgac taatgacatc ctaggcccat attctttgtc 60

gacgatgtgg tagatctagt gatactgaga cagtcagtag ttgcaatggc ctgctctcca 120

gagaaggatc agccctcc

139

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 45

cttacactga cactcggaga 20

<210> 46

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 46

ctactgccgt tcacctccac c 21

<210> 47

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 47

cggaagcttc caccatggcc tgctctccag agaaggatc 39

<210> 48

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 48

cggcttagac tactgccgtt cacctccacc tgg 33